PATTERNS OF GENETIC VARIATION AMONG ISLAND AND MAINLAND POPULATIONS OF NATIVE PELLITORY (*PARIETARIA DEBILIS*, URTICACEAE)

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ABSTRACT

Isozyme electrophoretic techniques were used to study patterns of genetic diversity within and between three island and two mainland populations of *Parietaria debilis*. With the exception of the Trigg population which was significantly different from all others the level of genetic divergence between populations was low and there was no obvious pattern in relation to genetic divergence between island and mainland populations. These data suggest that there are unlikely to be any detrimental effects resulting from gene exchange between original mainland populations and artificial mainland populations established from the more abundant island seed.

INTRODUCTION

Parietaria debilis has a cosmopolitan distribution and occurs in and adjacent to the Perth Metropolitan area in coastal sites, on islands and on granites of the Darling Scarp. Populations on Garden and Rottnest Islands have probably been isolated from the mainland for 6000 and 8000 thousand years respectively. Although there appears to be no morphological differences between mainland and island forms it is possible that prolonged isolation may have resulted in significant genetic divergence with the island populations now represented by distinct and possibly unique gene pools.

This may have important implications if new mainland populations are established with non local seed material from the larger and more accessible island populations (see Hopper and Coates, 1990; Ledig, 1986). There is increasing interest in growing this plant in cultivation, since it is the native food plant in south-western Australia of the Australian admiral butterfly (*Vanessa itea*) (Powell, 1993).

Population genetic studies using molecular markers such as isozymes have the potential to accurately determine the level of genetic divergence between populations or groups of populations within species. The technique of isozyme electrophoresis has proven to be a particularly cost effective means of producing reliable genetic markers that can be used to analyse patterns of genetic variation within and between plant populations (see

Soltis and Soltis 1989). The aim of this study was to investigate the levels of genetic differentiation between island and mainland populations of *P.debilis* by using isozyme electrophoretic techniques.

MATERIALS AND METHODS

Up to 50 seeds per population were germinated and seedling material prepared for isozyme analysis as described by Coates (1988). Isozyme methods were based on the Helena Laboratory cellulose acetate plate electrophoresis system (see Hebert and Beaton, 1989)

Fifteen enzyme systems were initially assayed: aspartate aminotransferase (AAT, E.C. 2.6.1.1), acid phosphatase (ACP, E.C. 3.1.3.2), alcohol dehydrogenase (ADH, E.C.,1.1.1.1), esterase (EST, E.C. 3.1.1.-), glucose 6 phosphate dehydrogenase (G6PDH) glutamate dehydrogenase (GDH, E.C. 1.4.1.2), isocitrate dehydrogenase (IDH, 1.1.1.42), lactate dehydrogenase (LDH, 1.1.1.27). leucine aminopeptidase (LAP, 3.4.17.1), malate dehydrogenase (MDH, 1.1.1.37), mannose-phosphate isomerase (MPI, E. C. 5.3.1.8), menadione reductase (MDR, E.C. 1.6.99.22)), 6 phosphogluconate dehydrogenase (6PGD, E.C. 1.1.1.44) phosphoglucose isomerase (PGI, E.C. E.C. 5.3.1.9), phosphoglucomutase (PGM, E.C. 2.7.5.1) shikimate dehydrogenase (SDH, E.C. 1.1.1.25). Of these six (AAT, MDH. MDR, 6PGD, PGI, PGM) gave reliable and reproducible results. In total, 10 zones of activity were scored and each zone was assumed to represent a single locus.

The average number of alleles per locus (*A*), percentage polymorphic loci (*P*), observed heterozygosity (*Ho*) and expected heterozygosity (*He*) were calculated as described by Brown and Weir (1983). The partitioning of genetic variation among populations was analysed using Nei's (1978) genetic distance (*D*). This was calculated for each pairwise combination of populations and a UPGMA phenogram constructed. The single locus diversity measures *A*, *P*, *He* and *Ho*, and *D*, were determined using the computer program BIOSYS-1 (Swofford and Selander, 1981). The UPGMA phenogram and standard errors for branch lengths were calculated as described by Ritland, 1989).

RESULTS

Three polymorphic loci were detected (*Pgi*–1, *Pgi*–2 and *Pgm*–1). This relatively low number of variable loci may be partly a reflection of the low level of genetic differentiation between populations but is probably also due to the difficulties in carrying out isozyme analysis of *P. debilis* material. Three alleles were detected at the *Pgi*–1 locus with the common allele occurring at a high frequency (0.83–0.98) in all populations. Two alleles were detected at the *Pgi*–2 locus and four at the *Pgm*–1 locus with both these loci showing some variation in allele frequencies between all populations (Table 1).

The single locus diversity measures (Table 2) provide only limited information because of the low number of loci analysed. They show, however, that the Trigg populations of *P. debilis* have relatively low levels of genetic diversity with fewer alleles detected per locus, and a

Table 1. Allele frequencies for the three polymorphic loci in the five populations of *P. debilis*

Locus/ Allele	Rottnest	Trigg	Burns Bch	Garden Is 1	Garden Is 2
	Population				
Pgi–1					
A	0.17	0.02	0.00	0.07	0.11
B	0.83	0.98	0.98	0.87	0.89
C	0.00	0.00	0.02	0.06	0.00
Pgi–2					
A	0.43	0.96	0.42	0.16	0.23
B	0.47	0.04	0.58	0.84	0.77
Pgm–1					
A	0.12	0.00	0.03	0.02	0.15
B	0.86	1.00	0.92	0.89	0.50
C	0.01	0.00	0.05	0.09	0.35
D	0.01	0.00	0.00	0.00	0.00

Table 2. Genetic variability based on single locus diversity measures *N* (mean sample size per locus), *A* (Average number of alleles per locus), *P* (percentage of loci polymorphic), *Ho*(observed heterozygosity) and *He* (expected heterozygosity or gene diversity index) (standard errors in parentheses)

Population	*N*	*A*	*P*	*Ho*	*He*
Rottnest	45.1	1.5 (0.30)	30.0	0.04 (0.02)	0.10 (0.06)
Trigg	22.2	1.2 (0.10)	20.0	0.00 (0.00)	0.01(0.01)
Burns Bch	45.2	1.4 (0.20)	30.0	0.02 (0.02)	0.07 (0.05)
Garden Is 1	34.4	1.5 (0.30)	30.0	0.06 (0.03)	0.07 (0.04)
Garden Is 2	36.5	1.4 (0.20)	30.0	0.11 (0.06)	0.12 (0.07)

significantly lower observed heterozygosity (*Ho*) and gene diversity index (*He*). The other populations all show similar levels of genetic diversity although they are generally lower than levels usually found in vascular plants (Hamrick and Godt, 1989).

Patterns of genetic differentiation between populations based on a UPGMA cluster analysis (Fig. 1) indicate no significant differentiation between the Rottnest, Burns Beach and Garden Island populations. Only the Trigg population shows some divergence from the other populations but as indicated below this is probably due to sampling error and the low level of genetic variation within that population rather than an indication of significant genetic differences. It is important to note that the standard error bars in Figure 1 are relatively large which shows that the overall divergence between populations is low. This is probably also a reflection of the low

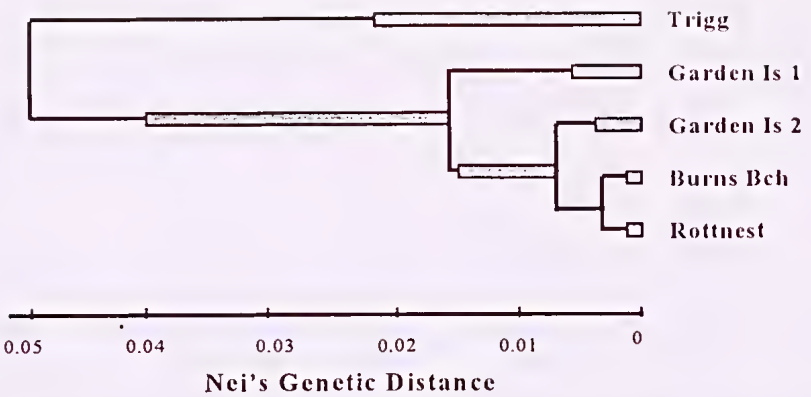

Figure 1. UPGMA clustering, with standard error bars for each branch length, based on Nei's (1978) genetic distance (*D*) between the populations of *P. debilis*. Branch lengths are significant if the standard error bar is less than half the branch length.

number of diagnostic isozyme markers available for analysis in *P. debilis*.

CONCLUSIONS

The isozyme analysis of the *P. debilis* material was not as detailed as was initially hoped. Of the fifteen isozyme systems screened for activity in *P. debilis* six gave reliable and reproducible results enabling the resolution of ten isozyme loci. The level of genetic divergence between all populations was generally low and there was no obvious pattern in relation to genetic divergence between island and mainland populations. Indeed the two Garden Island populations show greater between population divergence than the Rottnest, Burns Beach and Garden Island 2 populations.

The differences between the Trigg population and the other populations, both in terms of within population genetic diversity and divergence between populations, was unexpected given the closest population at Burns Beach shows no such differences. It seems likely that the distinct nature of the Trigg population is probably due to sampling error and small population size reflected in the significantly lower genetic diversity estimates (Table 2). Demographic data would be needed before any definite conclusion could be reached in relation to this population's reduced genetic variation and genetic uniqueness.

In conclusion there is no indication from these isozyme data to suggest that the establishment of artificial mainland populations of *P. debilis* using island material will have any detrimental effects, in terms of hybridisation and outbreeding depression, on any nearby natural mainland populations.

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